

P090

Differently expressed genes of soybean by ambient heat stress

Inuk Jung¹⁾, Jin Hyeon Kim²⁾ and Woosuk Jung^{2)*}

¹⁾*Interdisciplinary Program in Bioinformatics, Seoul National University, Gwanak-Gu, Seoul, Republic of Korea,*

²⁾*Department of Crop Science, Sanghuh College of Life Sciences, Konkuk University, Gwangjin-Gu, Seoul*

*Corresponding author

Abstract

Plants are grown under constitutive changing of environmental conditions and response to external conditions at both protein and transcription level. The effects of heat on plant growth are broad and influence the yield directly. Heat stresses could be classified depend on intensity and duration. Fundamental changes of growth condition by climate change maybe or maybe not classified as a stress on plant growth. The effects of a short and unanticipated impact of elevated heat on plant could be different with those of under longer extension of ambient heat. To examine differently expressed gene sets by ambient heat stress of soybean, we grow the soybean in normal condition for three weeks. After that, soybean plants move to growth chamber. The temperature of growth chamber increase up to 9 °C for four days. We have extracted mRNA and micro RNA every 24 hours and carried RNA sequence analysis. We found major metabolic pathways affected by ambient heat stress. Mainly carbon metabolism, translation machinery and amino acid synthesis are affected. We discussed the expression patterns of genes of heat sensing and hormone responses.

Keywords: ambient heat stress, soybean, RNA sequence analysis

Acknowledgement

This work was supported by Agenda project PJ011425022017, RDA, Korea.

Corresponding author*

Woosuk Jung

Address: Department of Crop Science, Sanghuh College of Life Sciences, Konkuk University, 120 Neungdong-ro, Gwangjin-gu, Seoul Korea.

Tel.: +82-02-450-3729

E-mail:jungw@konkuk.ac.kr